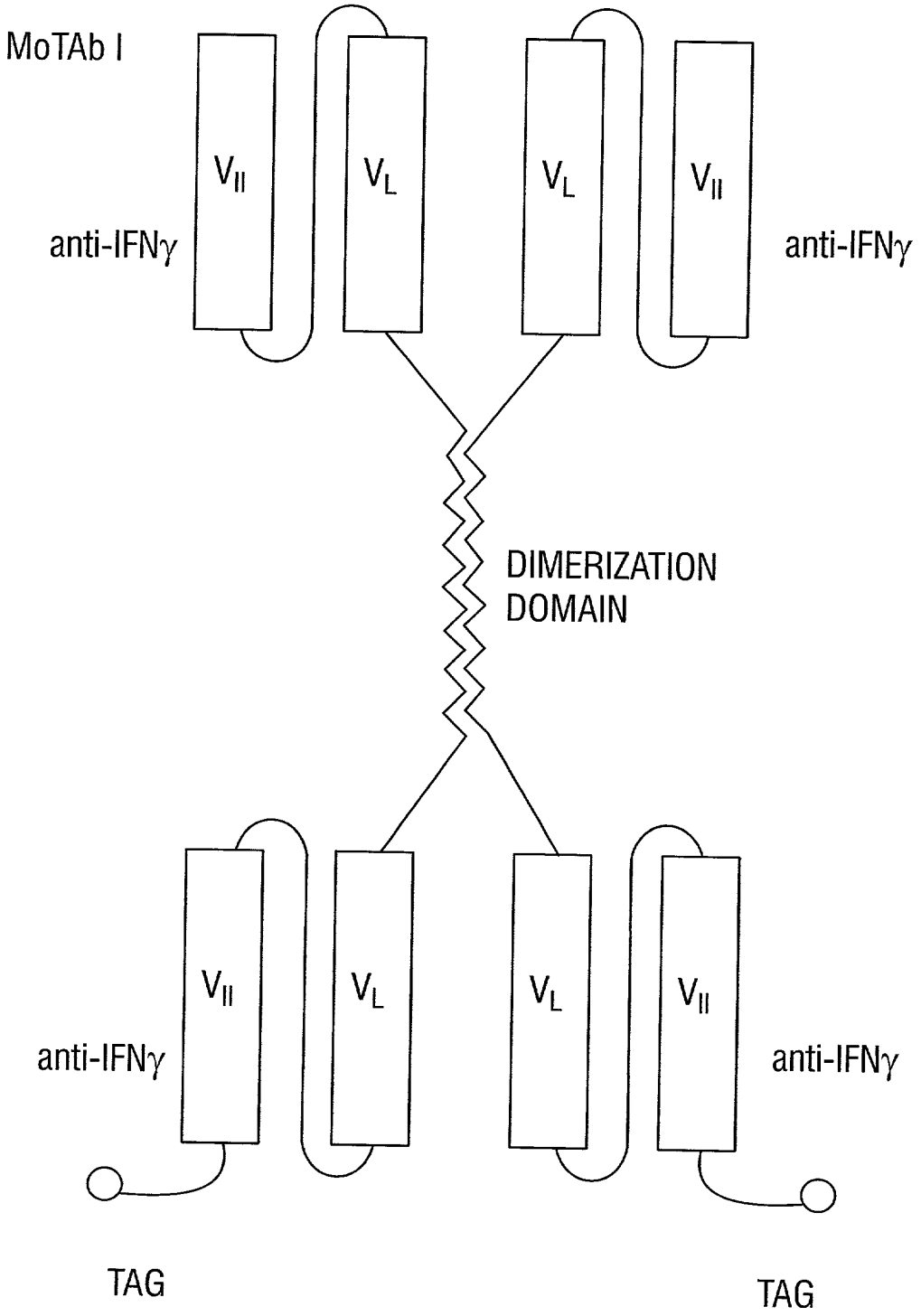


FIG. 1A

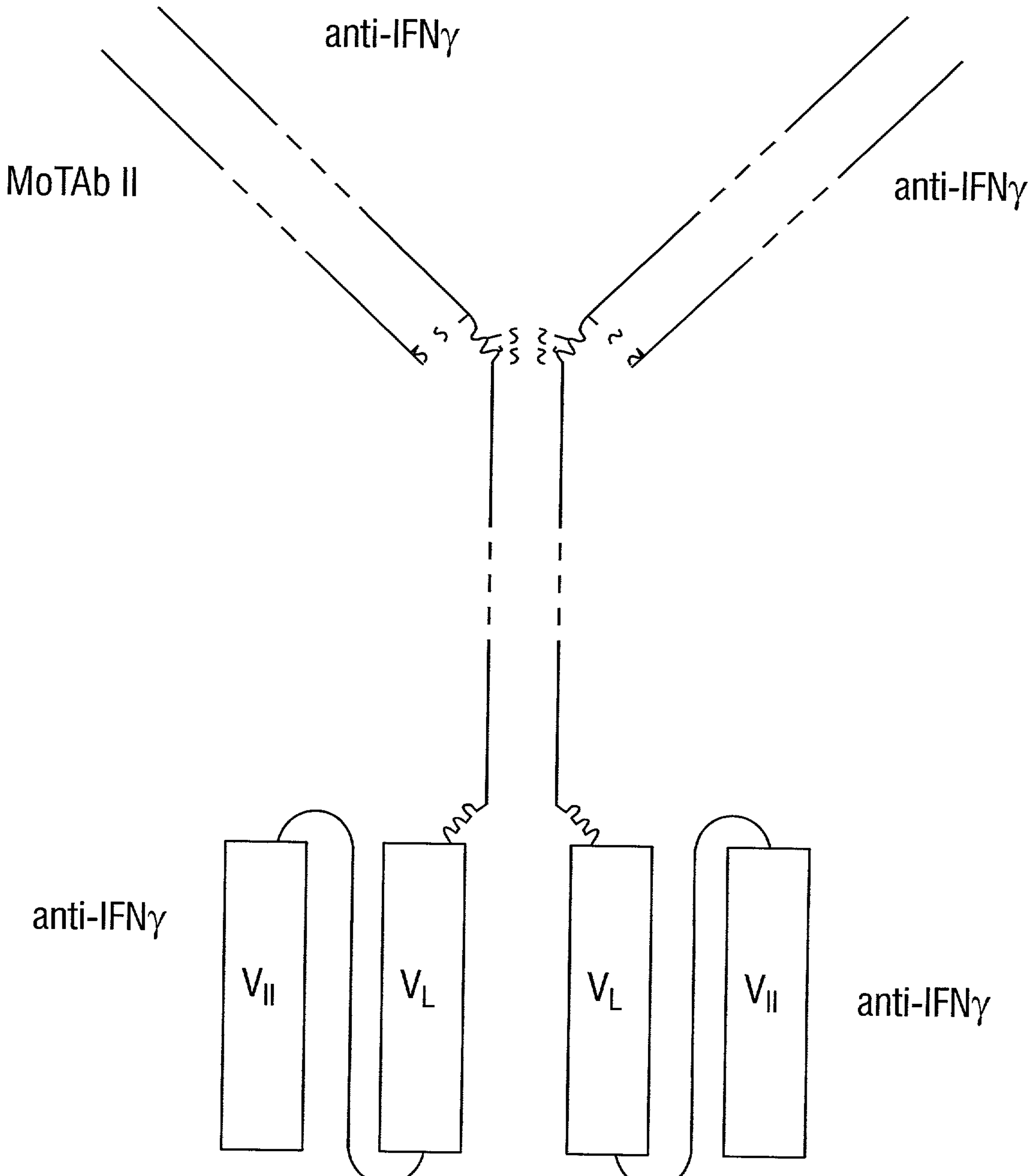


FIG. 1B

ATG AAA TAC CTA TTG CCT ACG GCA GCC GCT GGA TTG TTA TTA CTC
MET Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu

GCT GCC CAA CCA GCG ATG GCC CAG GTG CAG CTG GTG CAG AGC GGT
Ala Ala Gln Pro Ala MET Ala Gln Val Gln Leu **Val** Gln Ser Gly

AGC GAA CTG AAA AAA CCG GGT GCG AGC GTT AAG ATC AGC TGC AAA
Ser Glu Leu Lys Lys Pro Gly **Ala** **Ser** Val Lys Ile Ser Cys Lys

CDR1

GCG AGC GGT TAT ACC TTC ACC GAT TAC GGT ATG AAC TGG GTT AAA
Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Gly MET Asn Trp Val Lys

CAG GCG CCG GGT CAA GGT CTG AAA TGG ATG GGT TGG ATC AAC ACC
Gln Ala Pro Gly Gln Gly Leu Lys Trp MET Gly Trp Ile Asn Thr

CDR2

TAC ACC GGT GAA AGC ACC TAC GTT GAC GAT TTC AAA GGT CGT TTC
Tyr Thr Gly Glu Ser Thr Tyr Val Asp Asp Phe Lys Gly Arg Phe

GTT TTC AGC CTG GAT ACC AGC GTT AGC GCG GCC TAC CTG CAG ATC
Val Phe Ser Leu **Asp** Thr Ser **Val** Ser Ala Ala Tyr Leu Gln Ile

AGC TCT CTG AAA GCG GAA GAC ACC GCG ACC TAC TTC TGC GCG CGT
Ser **Ser** Leu Lys **Ala** Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg

CDR3

CGC GGT TTC TAC GCG ATG GAT TAC TGG GGC CAA GGG ACC ACG GTC
Arg Gly Phe Tyr Ala MET Asp Tyr Trp Gly Gln Gly Thr Thr Val

Linker

ACC GTC TCC TCA GGT GGA GGC GGT TCA GGC GGA GGT GGC TCT GGC
Thr Val Ser Ser **Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly**
GGT GGC GGA TCG GAC ATC GTA CTG ACC CAG AGC CCG GCG ACC ATG
Gly Gly Gly Ser Asp Ile **Val** Leu Thr Gln Ser Pro Ala **Thr** MET

AGC GCG AGC CCG GGT GAA CGT GTT ACC CTG ACC TGC AGC GCG AGC
Ser Ala Ser Pro Gly Glu **Arg** Val Thr Leu Thr Cys Ser Ala Ser

FIG. 2A

CDR1

TCT AGC ATC AGC TAT ATG TTC TGG TAT CAT CAG CGT CCG GGT CAG
Ser Ser Ile Ser Tyr MET Phe Trp Tyr His Gln Arg Pro Gly **Gln**

CDR2

AGC CCG CGT CTG TTG ATC TAT GAT ACC AGC AAC CTG GCG AGC GGT
Ser Pro Arg Leu Leu Ile Tyr Asp Thr Ser Asn Leu Ala Ser Gly

GTT CCG GCG CGT TTC AGC GGT AGC GGT AGC GGT ACC AGC TAT AGC
Val Pro **Ala** Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser

CTG ACC ATC AGC CGT ATG GAA CCG GAA GAT TTC GCG ACC TAT TTC
Leu Thr Ile Ser Arg MET Glu **Pro** Glu Asp **Phe** Ala Thr Tyr Phe

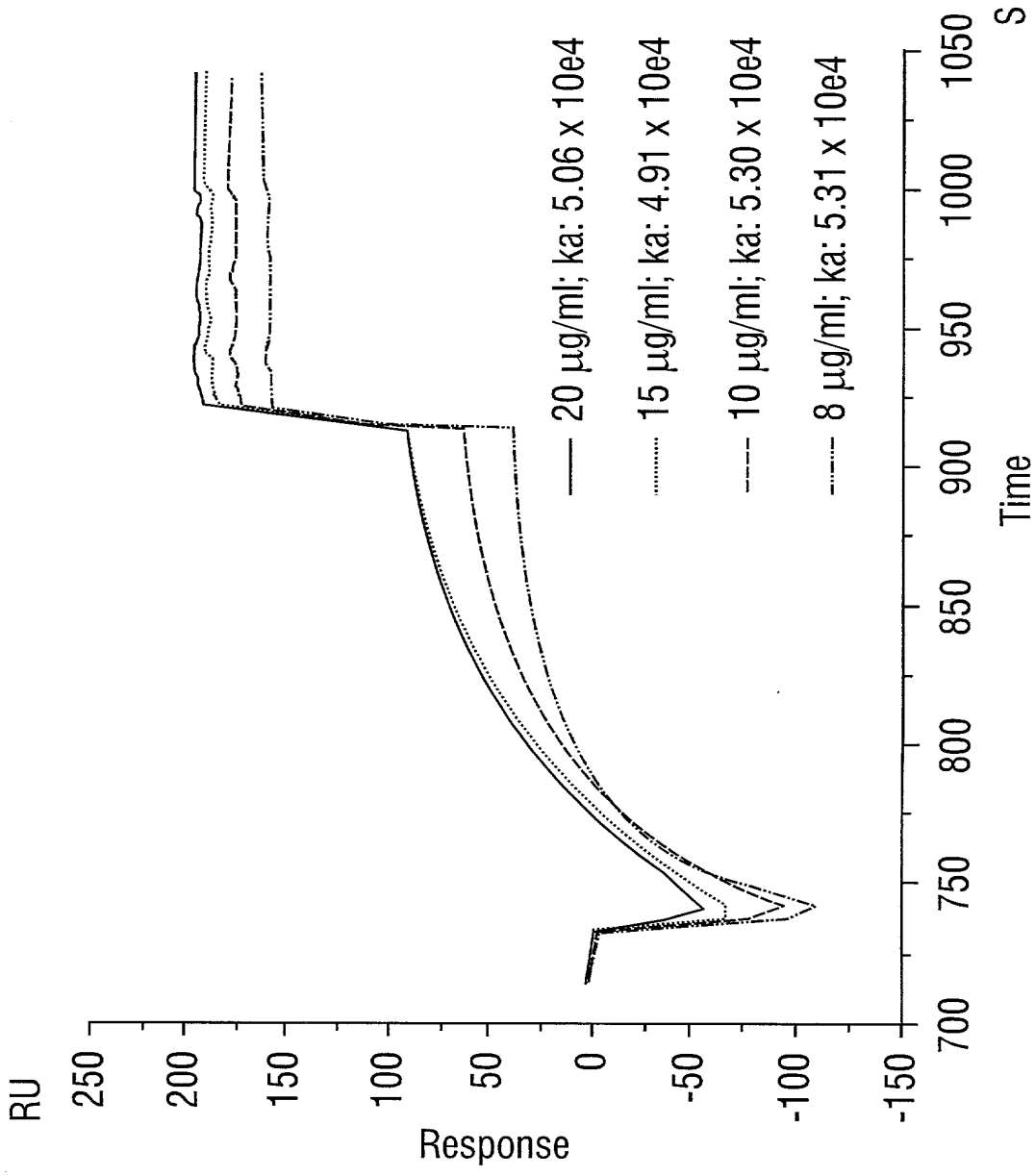
CDR3

TGC CAT CAG AGC TCT AGC TAT CCG TTC ACC TTC GGT CAG GGT ACC
Cys His Gln Ser Ser Ser Tyr Pro Phe Thr Phe Gly **Gln** Gly Thr

His6-Tag

AAA CTC GAG ATC AAA CGG CAC CAT CAC CAT CAC CAC TAA
Lys Leu Glu Ile Lys Arg **His His His His His His** ---

FIG. 2B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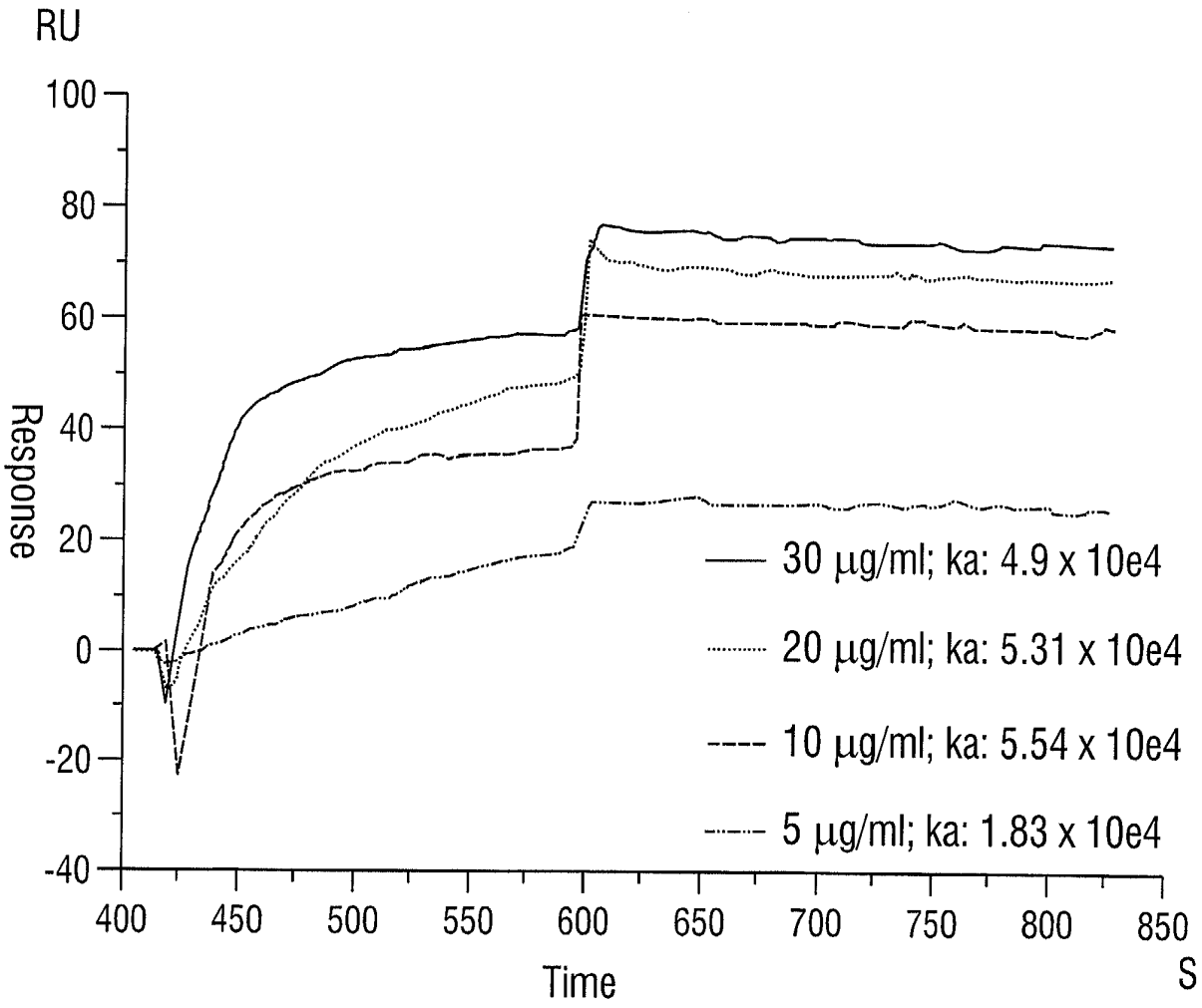
250
200
150
100
50
0
-50
-100
-150
Response
700
750
800
850
900
950
1000
1050
Time
S
20 µg/ml; ka: 5.06 x 10e4
15 µg/ml; ka: 4.91 x 10e4
10 µg/ml; ka: 5.30 x 10e4
8 µg/ml; ka: 5.31 x 10e4

FIG. 3


RU
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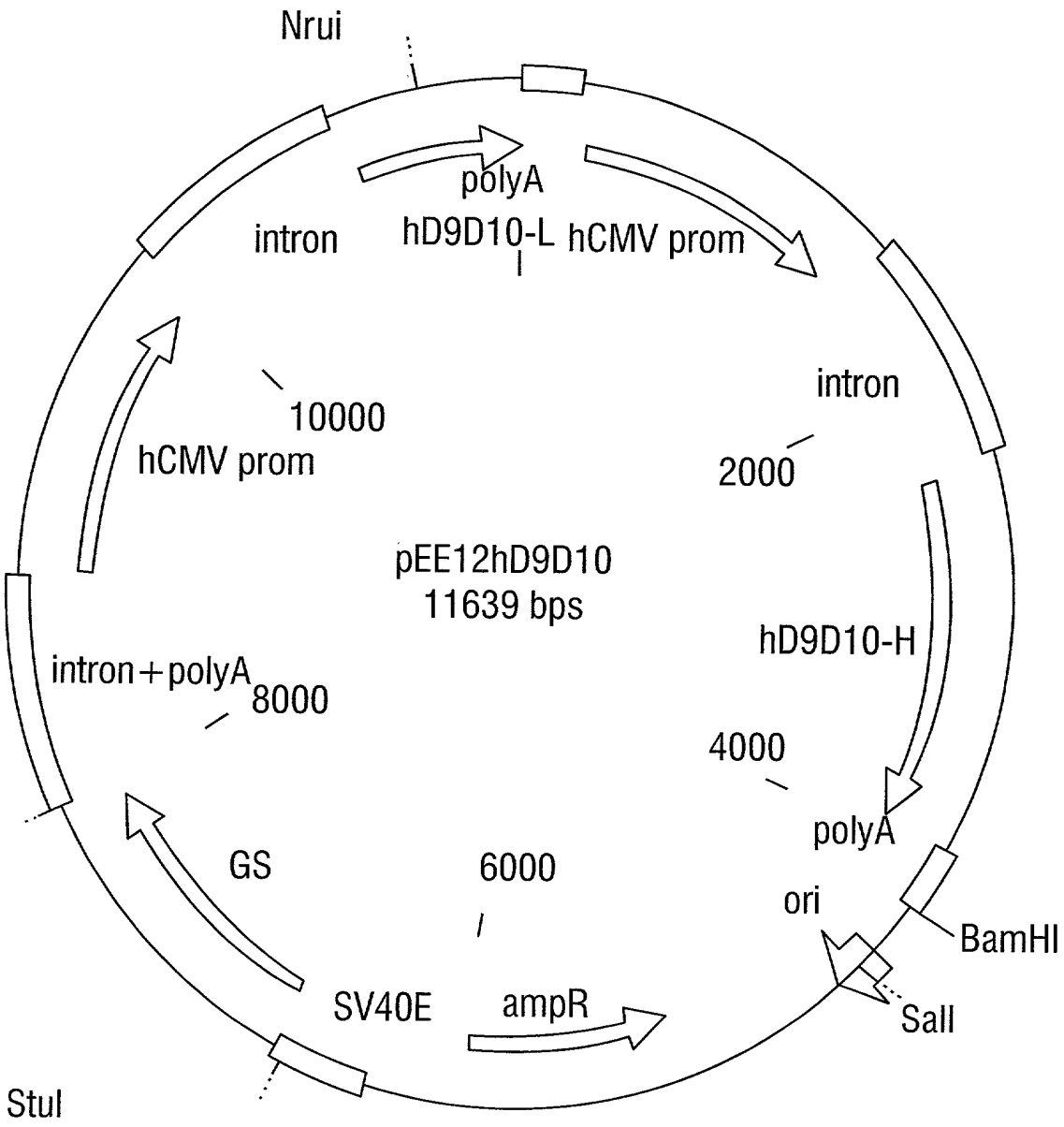
80
60
40
20
0
-20
-40
Response
400
450
500
550
600
650
700
750
800
850
Time
S
30 µg/ml; ka: 4.9 x 10e4
20 µg/ml; ka: 5.31 x 10e4
10 µg/ml; ka: 5.54 x 10e4
5 µg/ml; ka: 1.83 x 10e4

FIG. 4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intron
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hCMV prom
intron
10000
hCMV prom
2000
pEE12hD9D10
11639 bps
hD9D10-H
intron+polyA
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4000
polyA
GS
6000
ori
BamHI
SV40E
ampR
SalI
StuI

FIG. 5

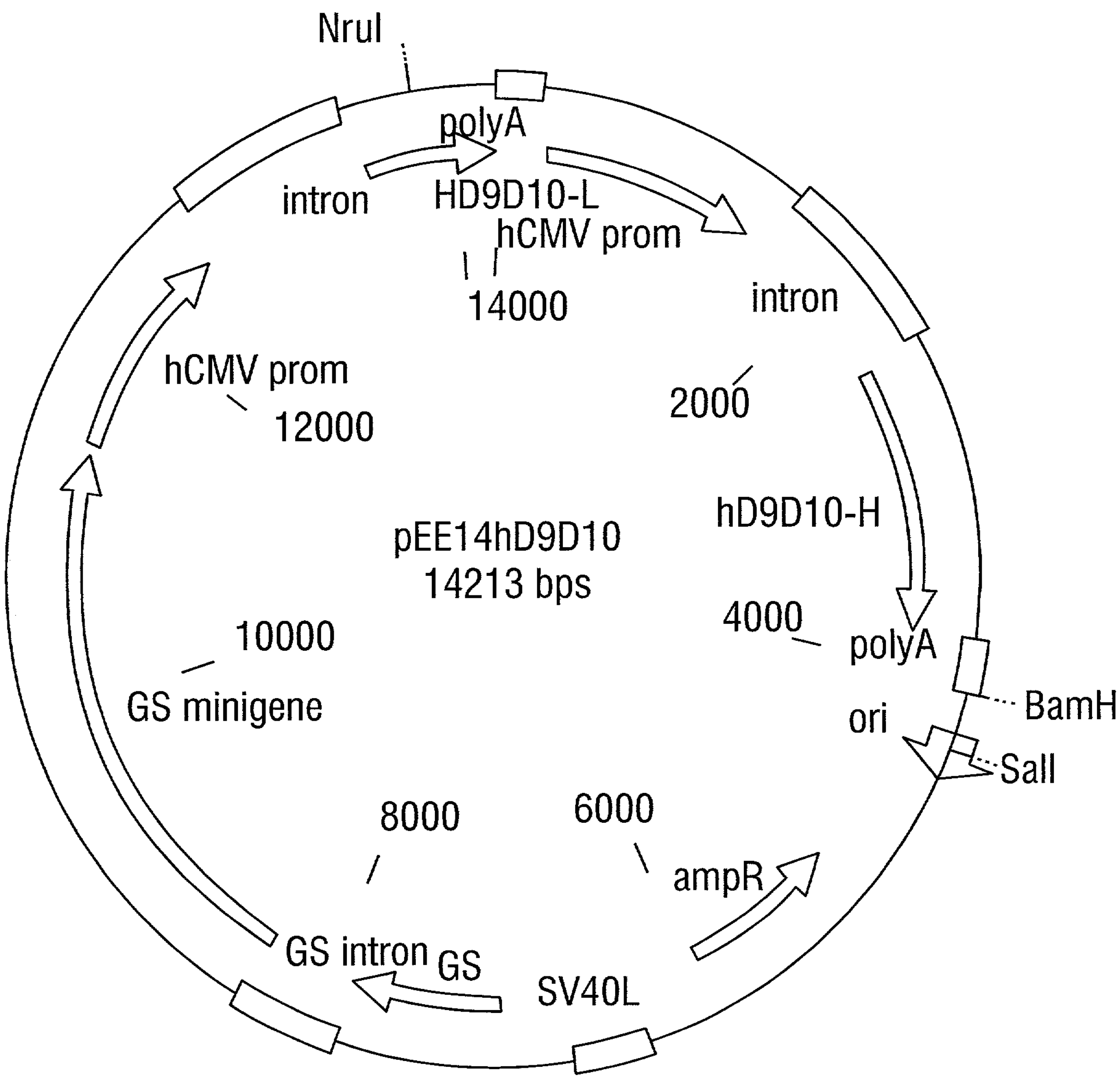


FIG. 6

1 ATGGATTTTCAAGTGCAGATTTTCAGCTTCCTGCTAATCA
41 GTGCCTCAGTCATACTCTCGCAGGTGCAGCTGGTGCAGAG
81 CGGTAGCGAACTGAAAAAACCGGGTGCGAGCGTTAAGATC
121 AGCTGCAAAGCGAGCGGTTATACCTTCACCGATTACGGTA
161 TGAACTGGGTTAAACAGGCGCCGGGTCAAGGTCTGAAATG
201 GATGGGTTGGATCAACACCTACACCGGTGAAAGCACCTAC
241 GTTGACGATTTCAAAGGTCGTTTCGTTTTCAGCCTGGATA
281 CCAGCGTTAGCGCGGCCTACCTGCAGATCAGCTCTCTGAA
321 AGCGGAAGACACCGCGACCTACTTCTGCGCGCGTCGCGGT
361 TTCTACGCGATGGATTACTGGGGCCAAGGGACCACGGTCA
401 CCGTCTCGAGCGCATCCACCAAGGGCCCATCGGTCTTCCC
441 CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
481 GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG
521 TGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT
561 GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC
601 TCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGG
641 GCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAG
681 CAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGT
721 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC
761 TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACC
801 CAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA
841 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA
881 AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC
921 CAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC
961 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC
1001 TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
1041 CCTCCCAGCCTCCATCGAGAAAACCATCTCCAAAGCCAAA
1081 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCAT
1121 CCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTG
1161 CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG
1201 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA
1241 CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTA
1281 TAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG
1321 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACA
1361 ACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA
1401 GCTT

FIG. 7

```
  1 ATGGATTTTCAAGTGCAGATTTTCAGCTTCCTGCTAATCA
 41 GTGCCTCAGTCATACTCTCGGACATCGAGCTGACCCAGAG
 81 CCCGGCGACCATGAGCGCGAGCCCGGGTGAACGTGTTACC
121 CTGACCTGCAGCGCGAGCTCTAGCATCAGCTATATGTTCT
161 GGTATCATCAGCGTCCGGGTCAGAGCCCGCGTCTGTTGAT
201 CTATGATACCAGCAACCTGGCGAGCGGTGTTCCGGCGCGT
241 TTCAGCGGTAGCGGTAGCGGTACCAGCTATAGCCTGACCA
281 TCAGCCGTATGGAACCGGAAGATTTCGCGACCTATTTCTG
321 CCATCAGAGCTCTAGCTATCCGTTCACCTTCGGTCAGGGT
361 ACCAAACTCGAGATCAAACGGACTGTGGCTGCACCATCTG
401 TCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGG
441 AACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCC
481 AGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCC
521 AATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAG
561 CAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTG
601 AGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCG
641 AAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAG
681 CTTCAACAGGGGAGAGTGC
```

FIG. 8

					5					10					15					20
1	M	D	F	Q	V	Q	I	F	S	F	L	L	I	S	A	S	V	I	L	S
21	Q	V	Q	L	V	Q	S	G	S	E	L	K	K	P	G	A	S	V	K	I
41	S	C	K	A	S	G	Y	T	F	T	D	Y	G	M	N	W	V	K	Q	A
61	P	G	Q	G	L	K	W	M	G	W	I	N	T	Y	T	G	E	S	T	Y
81	V	D	D	F	K	G	R	F	V	F	S	L	D	T	S	V	S	A	A	Y
101	L	Q	I	S	S	L	K	A	E	D	T	A	T	Y	F	C	A	R	R	G
121	F	Y	A	M	D	Y	W	G	Q	G	T	T	V	T	V	S	S	A	S	T
141	K	G	P	S	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A
161	A	L	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S
181	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G	L	Y
201	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q	T	Y	I	C
221	N	V	N	H	K	P	S	N	T	K	V	D	K	R	V	E	P	K	S	C
241	D	K	T	H	T	C	P	P	C	P	A	P	E	L	L	G	G	P	S	V
261	F	L	F	P	P	K	P	K	D	T	L	M	I	S	R	T	P	E	V	T
281	C	V	V	V	D	V	S	H	E	D	P	E	V	K	F	N	W	Y	V	D
301	G	V	E	V	H	N	A	K	T	K	P	R	E	E	Q	Y	N	S	T	Y
321	R	V	V	S	V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K
341	C	K	V	S	N	K	A	L	P	A	S	I	E	K	T	I	S	K	A	K
361	G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	E	E	M	T	K
381	N	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D	I	A	V	E
401	W	E	S	N	G	Q	P	E	N	N	Y	K	T	T	P	P	V	L	D	S
421	D	G	S	F	F	L	Y	S	K	L	T	V	D	K	S	R	W	Q	Q	G
441	N	V	F	S	C	S	V	M	H	E	A	L	H	N	H	Y	T	Q	K	S
461	L	S	L	S	P	G	K	L												

FIG. 9

					5				10				15						20
1	M	D	F	Q	V	Q	I	F	S	F	L	L	I	S	A	S	V	I	L	S
21	D	I	E	L	T	Q	S	P	A	T	M	S	A	S	P	G	E	R	V	T
41	L	T	C	S	A	S	S	S	I	S	Y	M	F	W	Y	H	Q	R	P	G
61	Q	S	P	R	L	L	I	Y	D	T	S	N	L	A	S	G	V	P	A	R
81	F	S	G	S	G	S	G	T	S	Y	S	L	T	I	S	R	M	E	P	E
101	D	F	A	T	Y	F	C	H	Q	S	S	S	Y	P	F	T	F	G	Q	G
121	T	K	L	E	I	K	R	T	V	A	A	P	S	V	F	I	F	P	P	S
141	D	E	Q	L	K	S	G	T	A	S	V	V	C	L	L	N	N	F	Y	P
161	R	E	A	K	V	Q	W	K	V	D	N	A	L	Q	S	G	N	S	Q	E
181	S	V	T	E	Q	D	S	K	D	S	T	Y	S	L	S	S	T	L	T	L
201	S	K	A	D	Y	E	K	H	K	V	Y	A	C	E	V	T	H	Q	G	L
221	S	S	P	V	T	K	S	F	N	R	G	E	C							

FIG. 10

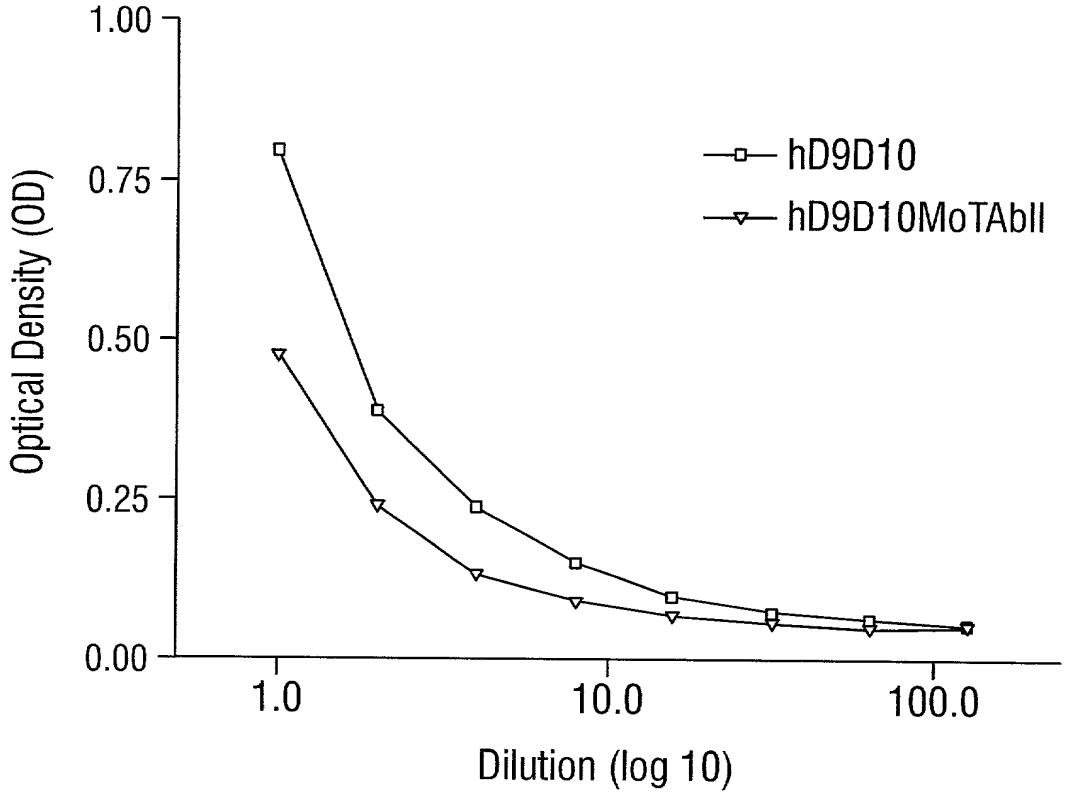
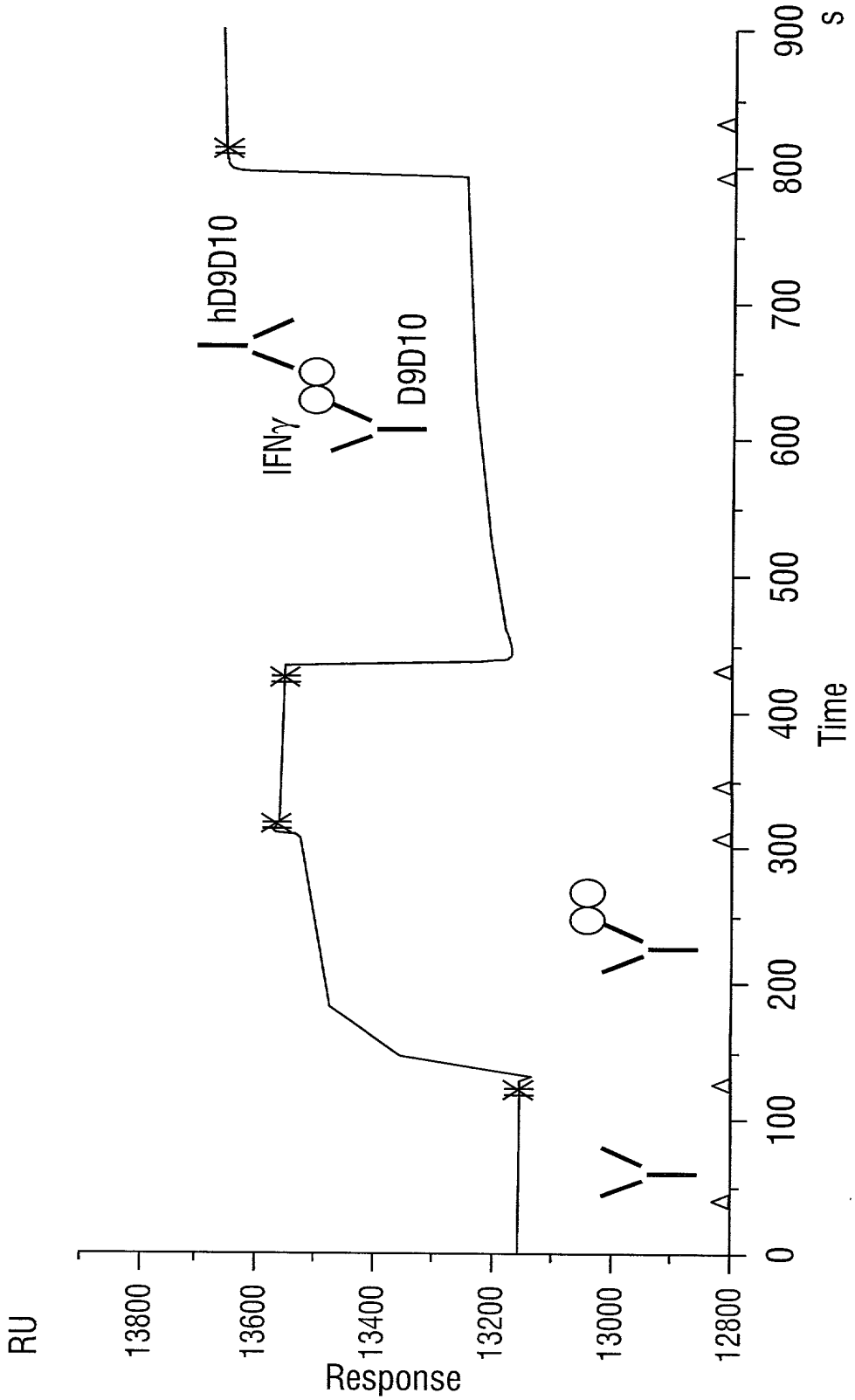


FIG. 11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100
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300
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500
600
700
800
900
Time
s
hD9D10
IFNγ
D9D10

FIG. 12

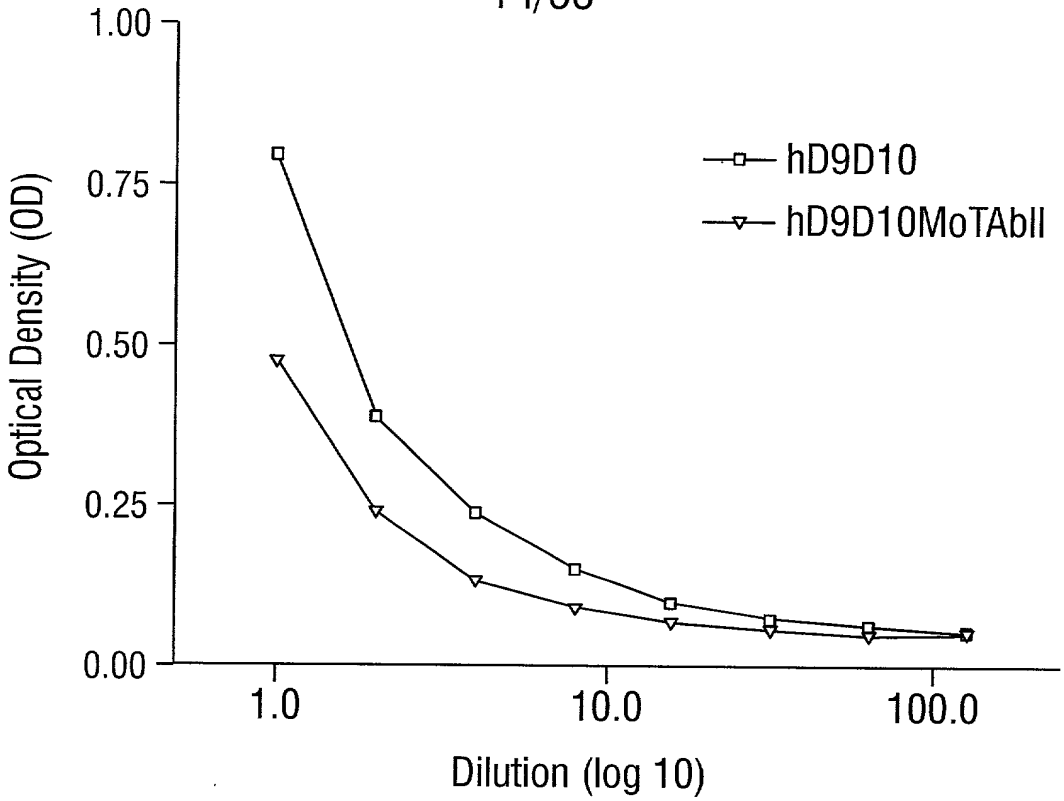


FIG. 13A

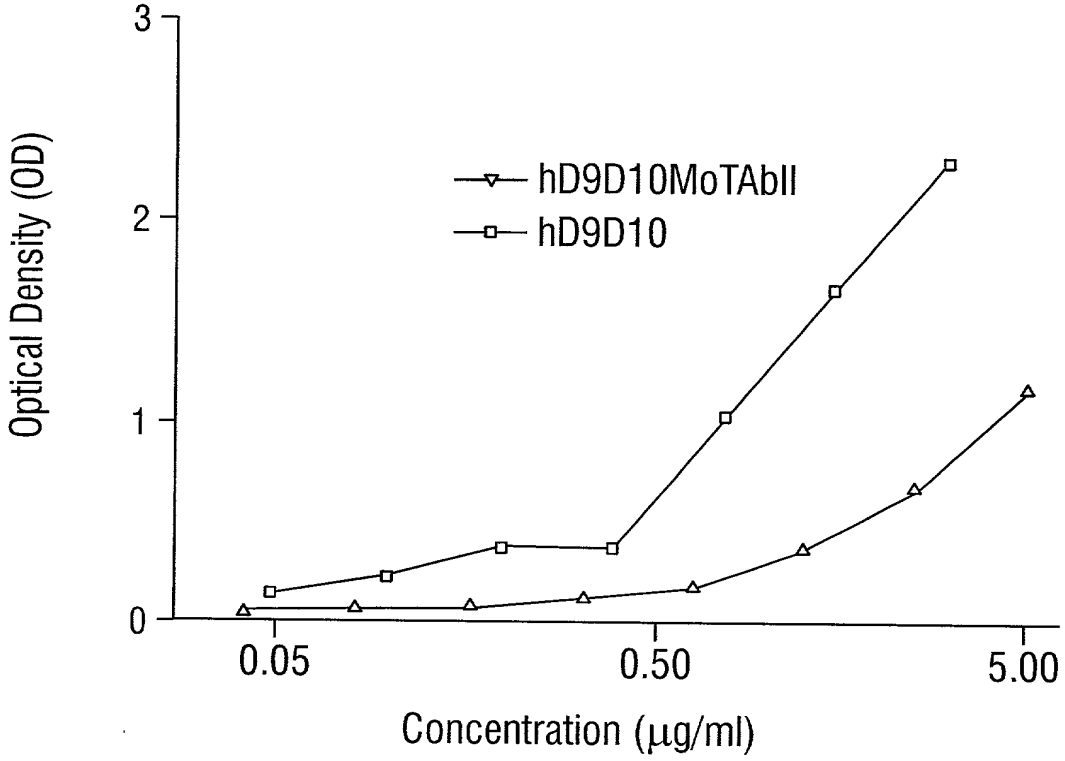
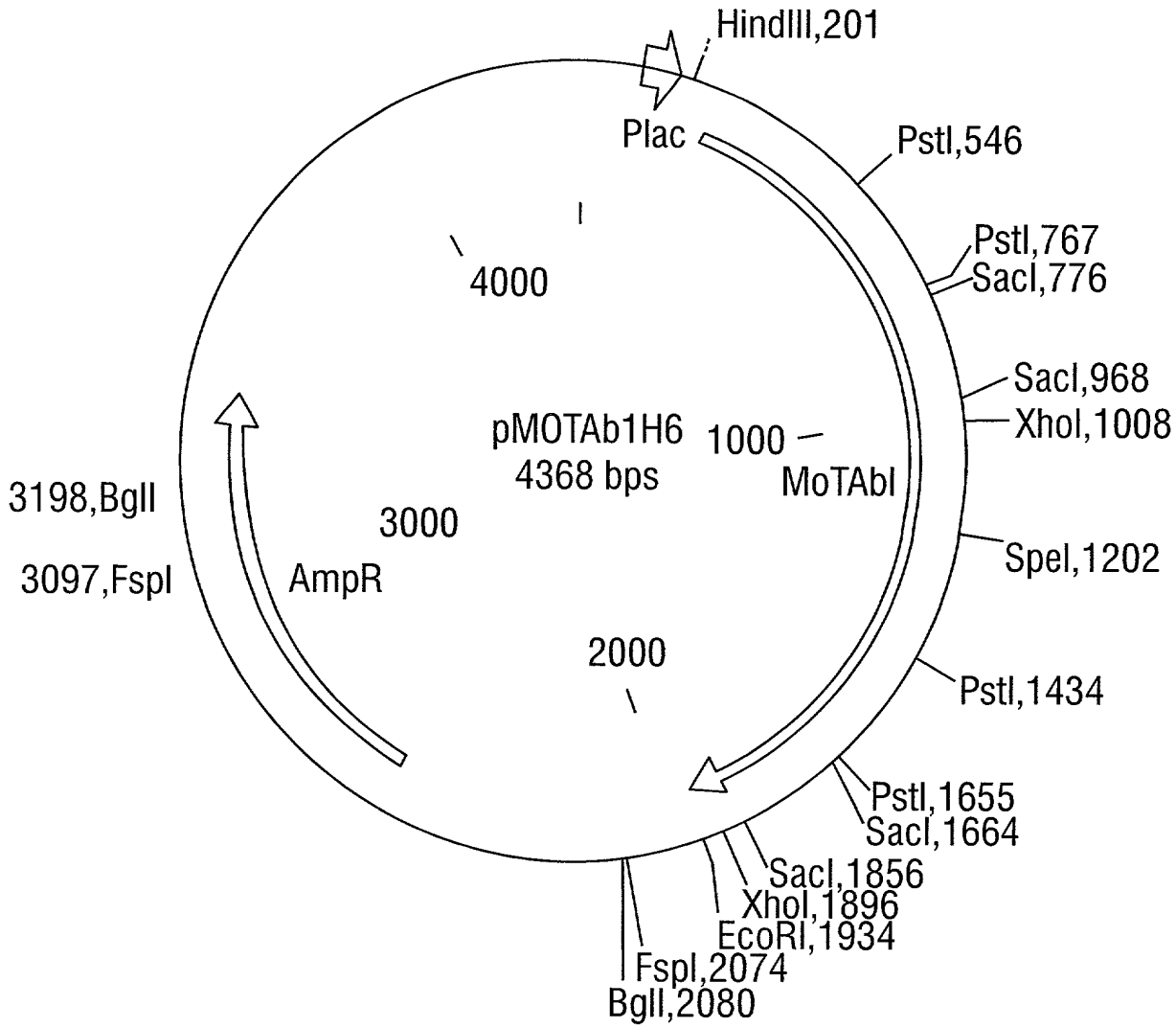


FIG. 13B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Plac
PstI,546
PstI,767
SacI,776
SacI,968
XhoI,1008
SpeI,1202
PstI,1434
PstI,1655
SacI,1664
SacI,1856
XhoI,1896
EcoRI,1934
FspI,2074
BglI,2080
4000
1000
2000
3000
pMOTAb1H6
4368 bps
MoTAbI
AmpR
3198,BglI
3097,FspI

FIG. 14

```
   1 CAGGTGCAGCTGGTGCAGAGCGGTAGCGAACTGAAAAAACCGGGTGCGAG
  51 CGTTAAGATCAGCTGCAAAGCGAGCGGTTATACCTTCACCGATTACGGTA
 101 TGAACTGGGTTAAACAGGCGCCGGGTCAAGGTCTGAAATGGATGGGTTGG
 151 ATCAACACCTACACCGGTGAAAGCACCTACGTTGACGATTTCAAAGGTCG
 201 TTTCGTTTTCAGCCTGGATACCAGCGTTAGCGCGGCCTACCTGCAGATCA
 251 GCTCTCTGAAAGCGGAAGACACCGCGACCTACTTCTGCGCGCGTCGCGGT
 301 TTCTACGCGATGGATTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTC
 351 AGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACA
 401 TCGTACTGACCCAGAGCCCGGCGACCATGAGCGCGAGCCCGGGTGAACGT
 451 GTTACCCTGACCTGCAGCGCGAGCTCTAGCATCAGCTATATGTTCTGGTA
 501 TCATCAGCGTCCGGGTCAGAGCCCGCGTCTGTTGATCTATGATACCAGCA
 551 ACCTGGCGAGCGGTGTTCCGGCGCGTTTCAGCGGTAGCGGTAGCGGTACC
 601 AGCTATAGCCTGACCATCAGCCGTATGGAACCGGAAGATTTCGCGACCTA
 651 TTTCTGCCATCAGAGCTCTAGCTATCCGTTCACCTTCGGTCAGGGTACCA
 701 AACTCGAGATCAAACGGACCCCGCTGGGTGATACCACTCATACCTCCGGA
 751 GGTGAACTGGAAGAGCTGTTGAAACATCTGAAAGAACTGCTGAAAGGTCC
 801 GCGGAAAGGTGAACTGGAGGAATTGCTGAAGCACCTGAAAGAGCTGTTGA
 851 AAGGTACCCCCCTGGGTGATACTACCCATACCAGCGGTCAGGTGCAACTA
 901 GTGCAGAGCGGTAGCGAACTGAAAAAACCGGGTGCGAGCGTTAAGATCAG
 951 CTGCAAAGCGAGCGGTTATACCTTCACCGATTACGGTATGAACTGGGTTA
1001 AACAGGCGCCGGGTCAAGGTCTGAAATGGATGGGTTGGATCAACACCTAC
1051 ACCGGTGAAAGCACCTACGTTGACGATTTCAAAGGTCGTTTCGTTTTCAG
1101 CCTGGATACCAGCGTTAGCGCGGCCTACCTGCAGATCAGCTCTCTGAAAG
1151 CGGAAGACACCGCGACCTACTTCTGCGCGCGTCGCGGTTTCTACGCGATG
1201 GATTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGAGGCGG
1251 TTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGTACTGACCC
1301 AGAGCCCGGCGACCATGAGCGCGAGCCCGGGTGAACGTGTTACCCTGACC
1351 TGCAGCGCGAGCTCTAGCATCAGCTATATGTTCTGGTATCATCAGCGTCC
1401 GGGTCAGAGCCCGCGTCTGTTGATCTATGATACCAGCAACCTGGCGAGCG
1451 GTGTTCCGGCGCGTTTCAGCGGTAGCGGTAGCGGTACCAGCTATAGCCTG
1501 ACCATCAGCCGTATGGAACCGGAAGATTTCGCGACCTATTTCTGCCATCA
1551 GAGCTCTAGCTATCCGTTCACCTTCGGTCAGGGTACCAAACTCGAGATCA
1601 AACGGCACCATCACCATCACCACTAA
```

FIG. 15

```
  1  QVQLVQSGSELKKPGASVKISCKASGYTFTDYGMNWVKQAPGQGLKWMGW
 51  INTYTGESTYVDDFKGRFVFSLDTSVSAAYLQISSLKAEDTATYFCARRG
101  FYAMDYWGQGTTVTVSSGGGGSGGGGSGGGGSDIVLTQSPATMSASPGER
151  VTLTCSASSSISYMFWYHQRPGQSPRLLIYDTSNLASGVPARFSGSGSGT
201  SYSLTISRMEPEDFATYFCHQSSSYPFTFGQGTKLEIKRTPLGDTTHTSG
251  GELEELLKHLKELLKGPRKGELEELLKHLKELLKGTPLGDTTHTSGQVQL
301  VQSGSELKKPGASVKISCKASGYTFTDYGMNWVKQAPGQGLKWMGWINTY
351  TGESTYVDDFKGRFVFSLDTSVSAAYLQISSLKAEDTATYFCARRGFYAM
401  DYWGQGTTVTVSSGGGGSGGGGSGGGGSDIVLTQSPATMSASPGERVTLT
451  CSASSSISYMFWYHQRPGQSPRLLIYDTSNLASGVPARFSGSGSGTSYSL
501  TISRMEPEDFATYFCHQSSSYPFTFGQGTKLEIKRHHHHHH
```

FIG. 16

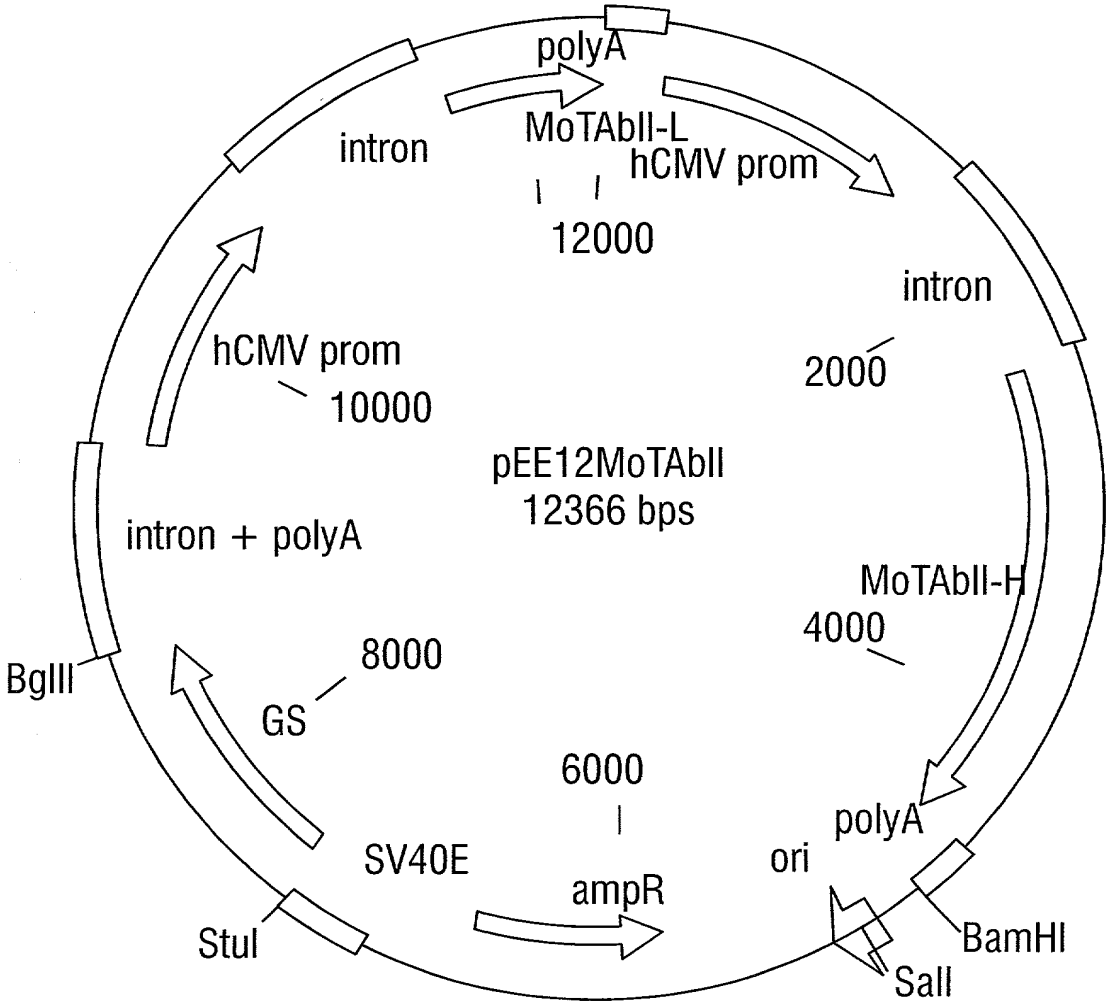
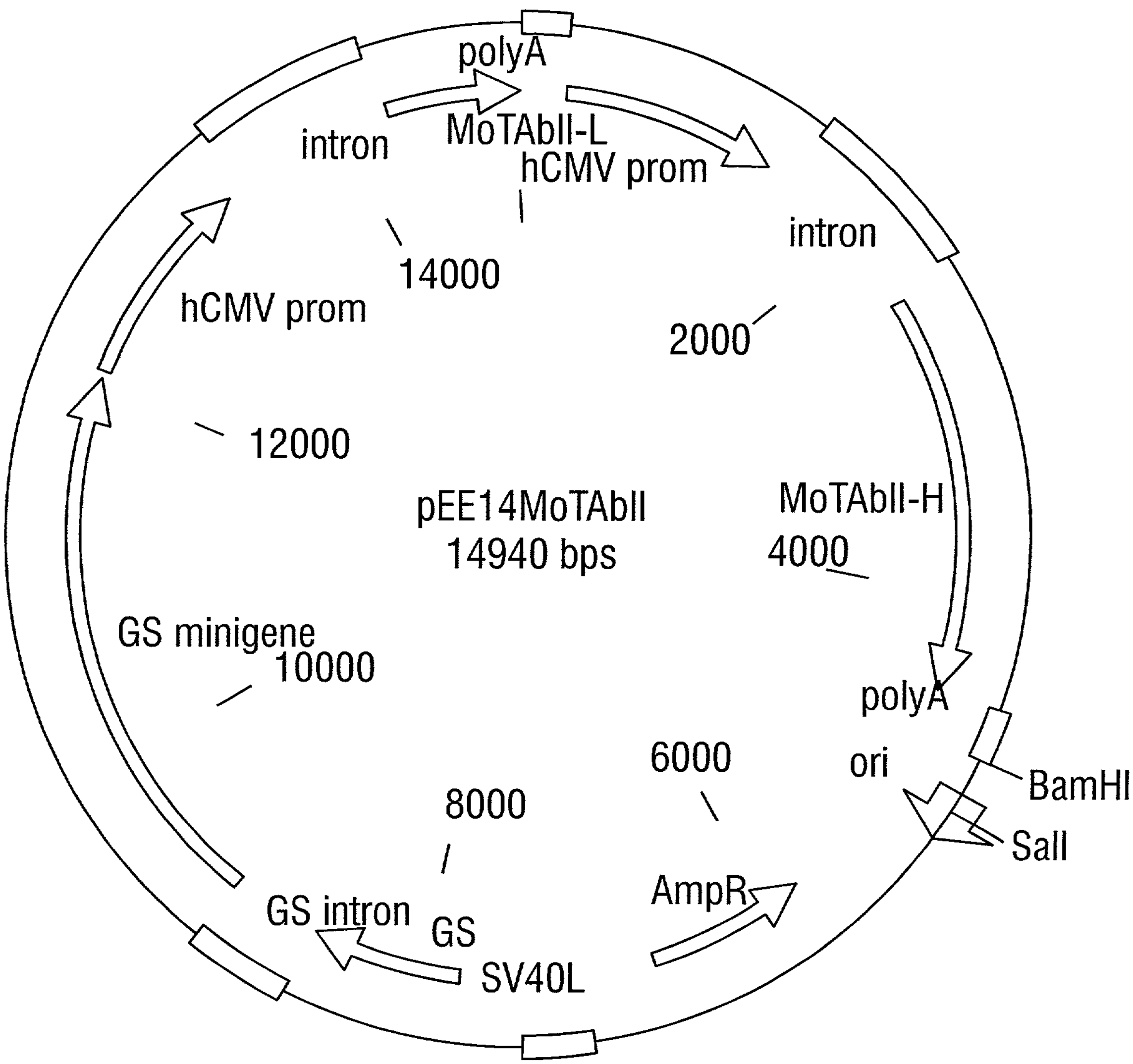


FIG. 17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MoTAbII-L
hCMV prom
intron
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hCMV prom
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12000
pEE14MoTAbII
14940 bps
MoTAbII-H
4000
GS minigene
10000
polyA
6000
ori
BamHI
8000
SalI
AmpR
GS intron
GS
SV40L

FIG. 18

```
1     ATGGATTTTCAAGTGCAGATTTTCAGCTTCCTGCTAATCA
41    GTGCCTCAGTCATACTCTCGCAGGTGCAGCTGGTGCAGAG
81    CGGTAGCGAACTGAAAAAACCGGGTGCGAGCGTTAAGATC
121   AGCTGCAAAGCGAGCGGTTATACCTTCACCGATTACGGTA
161   TGAACTGGGTTAAACAGGCGCCGGGTCAAGGTCTGAAATG
201   GATGGGTTGGATCAACACCTACACCGGTGAAAGCACCTAC
241   GTTGACGATTTCAAAGGTCGTTTCGTTTTCAGCCTGGATA
281   CCAGCGTTAGCGCGGCCTACCTGCAGATCAGCTCTCTGAA
321   AGCGGAAGACACCGCGACCTACTTCTGCGCGCGTCGCGGT
361   TTCTACGCGATGGATTACTGGGGCCAAGGGACCACGGTCA
401   CCGTCTCGAGCGCATCCACCAAGGGCCCATCGGTCTTCCC
441   CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
481   GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG
521   TGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT
561   GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC
601   TCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGG
641   GCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAG
681   CAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGT
721   GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC
761   TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACC
801   CAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA
841   TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA
881   AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC
921   CAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC
961   CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC
1001  TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
1041  CCTCCCAGCCTCCATCGAGAAAACCATCTCCAAAGCCAAA
1081  GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCAT
1121  CCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTG
1161  CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG
1201  TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA
1241  CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTA
1281  TAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG
1321  AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACA
```

FIG. 19A

```
1361 ACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA
1401 GCTTGGCGGAGGCTCACAGGTGCAGCTGGTGCAGAGCGGT
1441 AGCGAACTGAAAAAACCGGGTGCGAGCGTTAAGATCAGCT
1481 GCAAAGCGAGCGGTTATACCTTCACCGATTACGGTATGAA
1521 CTGGGTTAAACAGGCGCCGGGTCAAGGTCTGAAATGGATG
1561 GGTTGGATCAACACCTACACCGGTGAAAGCACCTACGTTG
1601 ACGATTTCAAAGGTCGTTTCGTTTTCAGCCTGGATACCAG
1641 CGTTAGCGCGGCCTACCTGCAGATCAGCTCTCTGAAAGCG
1681 GAAGACACCGCGACCTACTTCTGCGCGCGTCGCGGTTTCT
1721 ACGCGATGGATTACTGGGGCCAAGGGACCACGGTCACCGT
1761 CTCCTCAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGC
1801 GGTGGCGGATCGGACATCGTACTGACCCAGAGCCCGGCGA
1841 CCATGAGCGCGAGCCCGGGTGAACGTGTTACCCTGACCTG
1881 CAGCGCGAGCTCTAGCATCAGCTATATGTTCTGGTATCAT
1921 CAGCGTCCGGGTCAGAGCCCGCGTCTGTTGATCTATGATA
1961 CCAGCAACCTGGCGAGCGGTGTTCCGGCGCGTTTCAGCGG
2001 TAGCGGTAGCGGTACCAGCTATAGCCTGACCATCAGCCGT
2041 ATGGAACCGGAAGATTTCGCGACCTATTTCTGCCATCAGA
2081 GCTCTAGCTATCCGTTCACCTTCGGTCAGGGTACCAAACT
2121 CGAGATCAAACGG
```

FIG. 19B

					5					10					15					20
1	M	D	F	Q	V	Q	I	F	S	F	L	L	I	S	A	S	V	I	L	S
21	Q	V	Q	L	V	Q	S	G	S	E	L	K	K	P	G	A	S	V	K	I
41	S	C	K	A	S	G	Y	T	F	T	D	Y	G	M	N	W	V	K	Q	A
61	P	G	Q	G	L	K	W	M	G	W	I	N	T	Y	T	G	E	S	T	Y
81	V	D	D	F	K	G	R	F	V	F	S	L	D	T	S	V	S	A	A	Y
101	L	Q	I	S	S	L	K	A	E	D	T	A	T	Y	F	C	A	R	R	G
121	F	Y	A	M	D	Y	W	G	Q	G	T	T	V	T	V	S	S	A	S	T
141	K	G	P	S	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A
161	A	L	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S
181	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G	L	Y
201	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q	T	Y	I	C
221	N	V	N	H	K	P	S	N	T	K	V	D	K	R	V	E	P	K	S	C
241	D	K	T	H	T	C	P	P	C	P	A	P	E	L	L	G	G	P	S	V
261	F	L	F	P	P	K	P	K	D	T	L	M	I	S	R	T	P	E	V	T
281	C	V	V	V	D	V	S	H	E	D	P	E	V	K	F	N	W	Y	V	D
301	G	V	E	V	H	N	A	K	T	K	P	R	E	E	Q	Y	N	S	T	Y
321	R	V	V	S	V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K
341	C	K	V	S	N	K	A	L	P	A	S	I	E	K	T	I	S	K	A	K
361	G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	E	E	M	T	K
381	N	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D	I	A	V	E
401	W	E	S	N	G	Q	P	E	N	N	Y	K	T	T	P	P	V	L	D	S
421	D	G	S	F	F	L	Y	S	K	L	T	V	D	K	S	R	W	Q	Q	G
441	N	V	F	S	C	S	V	M	H	E	A	L	H	N	H	Y	T	Q	K	S
461	L	S	L	S	P	G	K	L	G	G	G	S	Q	V	Q	L	V	Q	S	G
481	S	E	L	K	K	P	G	A	S	V	K	I	S	C	K	A	S	G	Y	T
501	F	T	D	Y	G	M	N	W	V	K	Q	A	P	G	Q	G	L	K	W	M
521	G	W	I	N	T	Y	T	G	E	S	T	Y	V	D	D	F	K	G	R	F
541	V	F	S	L	D	T	S	V	S	A	A	Y	L	Q	I	S	S	L	K	A
561	E	D	T	A	T	Y	F	C	A	R	R	G	F	Y	A	M	D	Y	W	G
581	Q	G	T	T	V	T	V	S	S	G	G	G	G	S	G	G	G	G	S	G

FIG. 20A

601 G G G S D I V L T Q S P A T M S A S P G
621 E R V T L T C S A S S S I S Y M F W Y H
641 Q R P G Q S P R L L I Y D T S N L A S G
661 V P A R F S G S G S G T S Y S L T I S R
681 M E P E D F A T Y F C H Q S S S Y P F T
701 F G Q G T K L E I K R

FIG. 20B

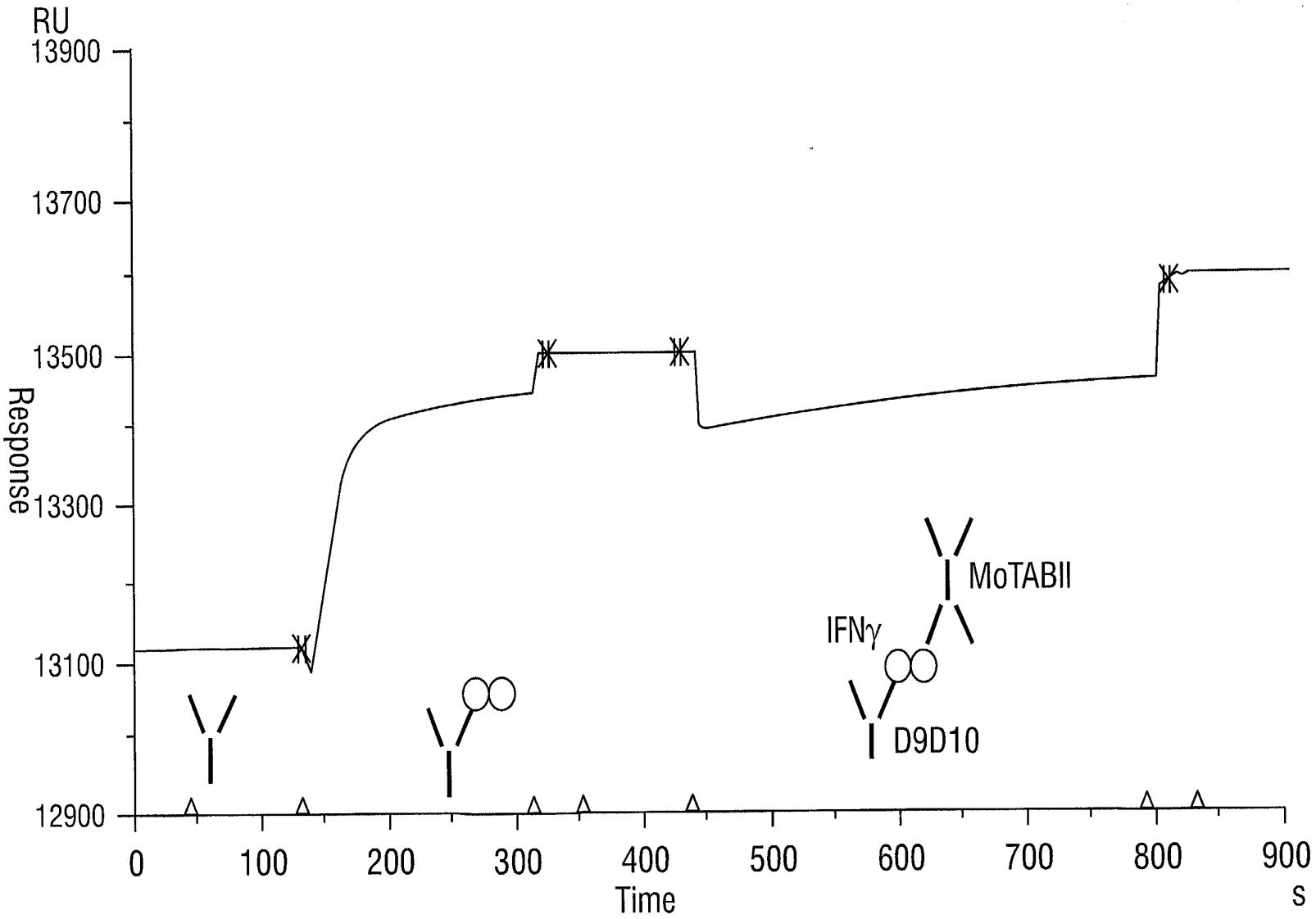

RU
13900
13700
13500
13300
13100
12900
Response
0
100
200
300
400
500
600
700
800
900
Time
s
MoTABII
IFNγ
D9D10

FIG. 21

1 QVQLVQSGSELKKPGASVKISCKASGYTFTDYGMNWVKQAPGQGLKWMGW
51 INTYTGESTYVDDFKGRFVFSLDTSVSAAYLQISSLKAEDTATYFCARRG
101 FYAMDYWGQGTTVTVSSGGGGSGGGGSDIVLTQSPATMSASPGERVTLTC
151 SASSSISYMFWYHQRPGQSPRLLIYDTSNLASGVPARFSGSGSGTSYSLT
201 ISRMEPEDFATYFCHQSSSYPFTFGQGTKLEIKRHHHHHH

FIG. 22

1 CAGGTGCAGCTGGTGCAGAGCGGTAGCGAACTGAAAAAACCGGGTGCGAG
51 CGTTAAGATCAGCTGCAAAGCGAGCGGTTATACCTTCACCGATTACGGTA
101 TGAACTGGGTTAAACAGGCGCCGGGTCAAGGTCTGAAATGGATGGGTTGG
151 ATCAACACCTACACCGGTGAAAGCACCTACGTTGACGATTTCAAAGGTCG
201 TTTCGTTTTCAGCCTGGATACCAGCGTTAGCGCGGCCTACCTGCAGATCA
251 GCTCTCTGAAAGCGGAAGACACCGCGACCTACTTCTGCGCGCGTCGCGGT
301 TTCTACGCGATGGATTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTC
351 AGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGTACTGACCCAGA
401 GCCCGGCGACCATGAGCGCGAGCCCGGGTGAACGTGTTACCCTGACCTGC
451 AGCGCGAGCTCTAGCATCAGCTATATGTTCTGGTATCATCAGCGTCCGGG
501 TCAGAGCCCGCGTCTGTTGATCTATGATACCAGCAACCTGGCGAGCGGTG
551 TTCCGGCGCGTTTCAGCGGTAGCGGTAGCGGTACCAGCTATAGCCTGACC
601 ATCAGCCGTATGGAACCGGAAGATTTCGCGACCTATTTCTGCCATCAGAG
651 CTCTAGCTATCCGTTCACCTTCGGTCAGGGTACCAAACTCGAGATCAAAC
701 GG

FIG. 23

1 QVQLVQSGSELKKPGASVKISCKASGYTFTDYGMNWVKQAPGQGLKWMGW
51 INTYTGESTYVDDFKGRFVFSLDTSVSAAYLQISSLKAEDTATYFCARRG
101 FYAMDYWGQGTTVTVSSGGGGSDIVLTQSPATMSASPGERVTLTCSASSS
151 ISYMFWYHQRPGQSPRLLIYDTSNLASGVPARFSGSGSGTSYSLTISRME
201 PEDFATYFCHQSSSYPFTFGQGTKLEIKRHHHHHH

FIG. 24

```
  1  CAGGTGCAGCTGGTGCAGAGCGGTAGCGAACTGAAAAAACCGGGTGCGAG
 51  CGTTAAGATCAGCTGCAAAGCGAGCGGTTATACCTTCACCGATTACGGTA
101  TGAACTGGGTTAAACAGGCGCCGGGTCAAGGTCTGAAATGGATGGGTTGG
151  ATCAACACCTACACCGGTGAAAGCACCTACGTTGACGATTTCAAAGGTCG
201  TTTCGTTTTCAGCCTGGATACCAGCGTTAGCGCGGCCTACCTGCAGATCA
251  GCTCTCTGAAAGCGGAAGACACCGCGACCTACTTCTGCGCGCGTCGCGGT
301  TTCTACGCGATGGATTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTC
351  AGGCGGTGGCGGATCGGACATCGTACTGACCCAGAGCCCGGCGACCATGA
401  GCGCGAGCCCGGGTGAACGTGTTACCCTGACCTGCAGCGCGAGCTCTAGC
451  ATCAGCTATATGTTCTGGTATCATCAGCGTCCGGGTCAGAGCCCGCGTCT
501  GTTGATCTATGATACCAGCAACCTGGCGAGCGGTGTTCCGGCGCGTTTCA
551  GCGGTAGCGGTAGCGGTACCAGCTATAGCCTGACCATCAGCCGTATGGAA
601  CCGGAAGATTTCGCGACCTATTTCTGCCATCAGAGCTCTAGCTATCCGTT
651  CACCTTCGGTCAGGGTACCAAACTCGAGATCAAACGG
```

FIG. 25

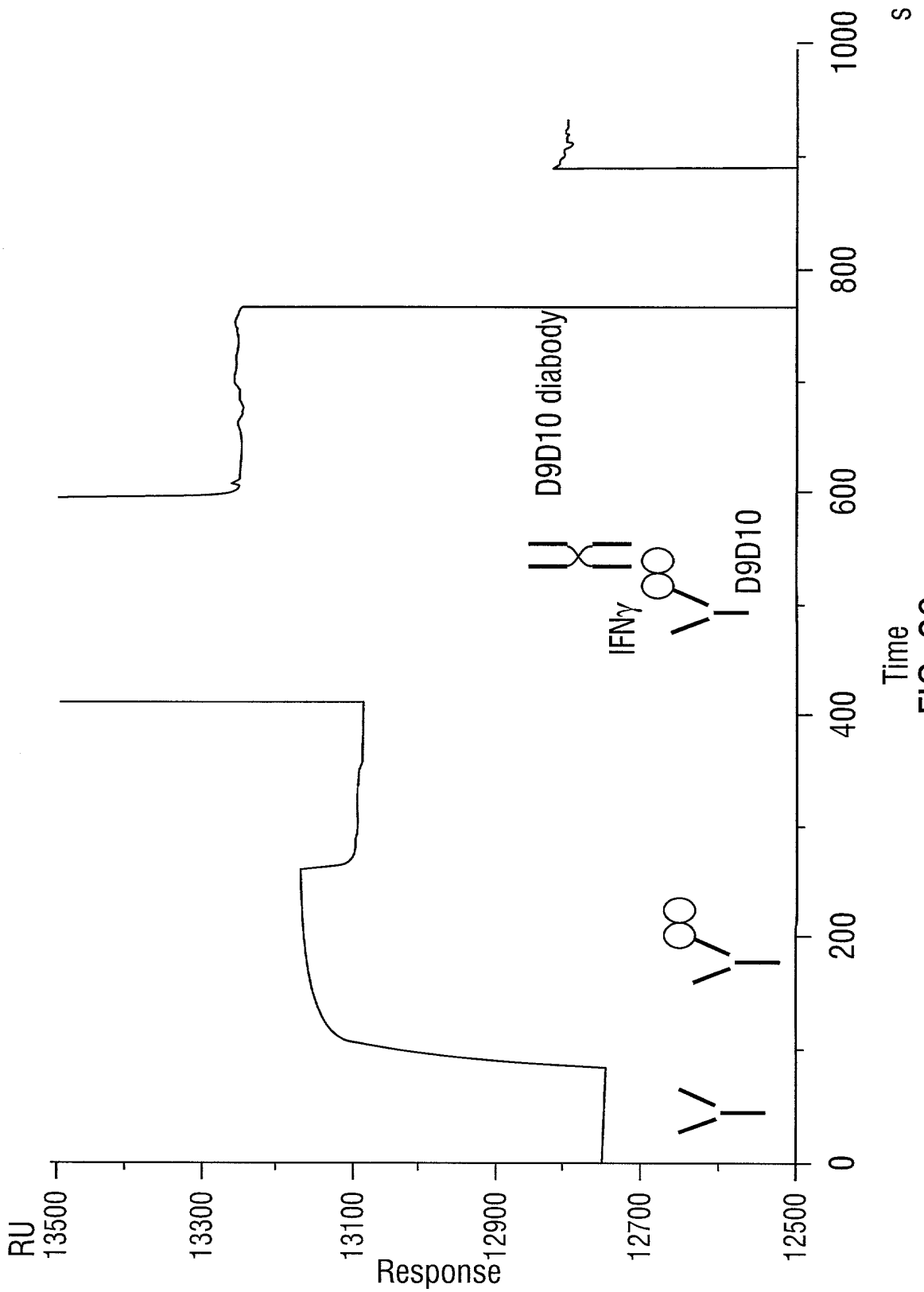

RU
13500
13300
13100
12900
12700
12500
Response
0
200
400
600
800
1000
s
Time
D9D10 diabody
IFNγ
D9D10

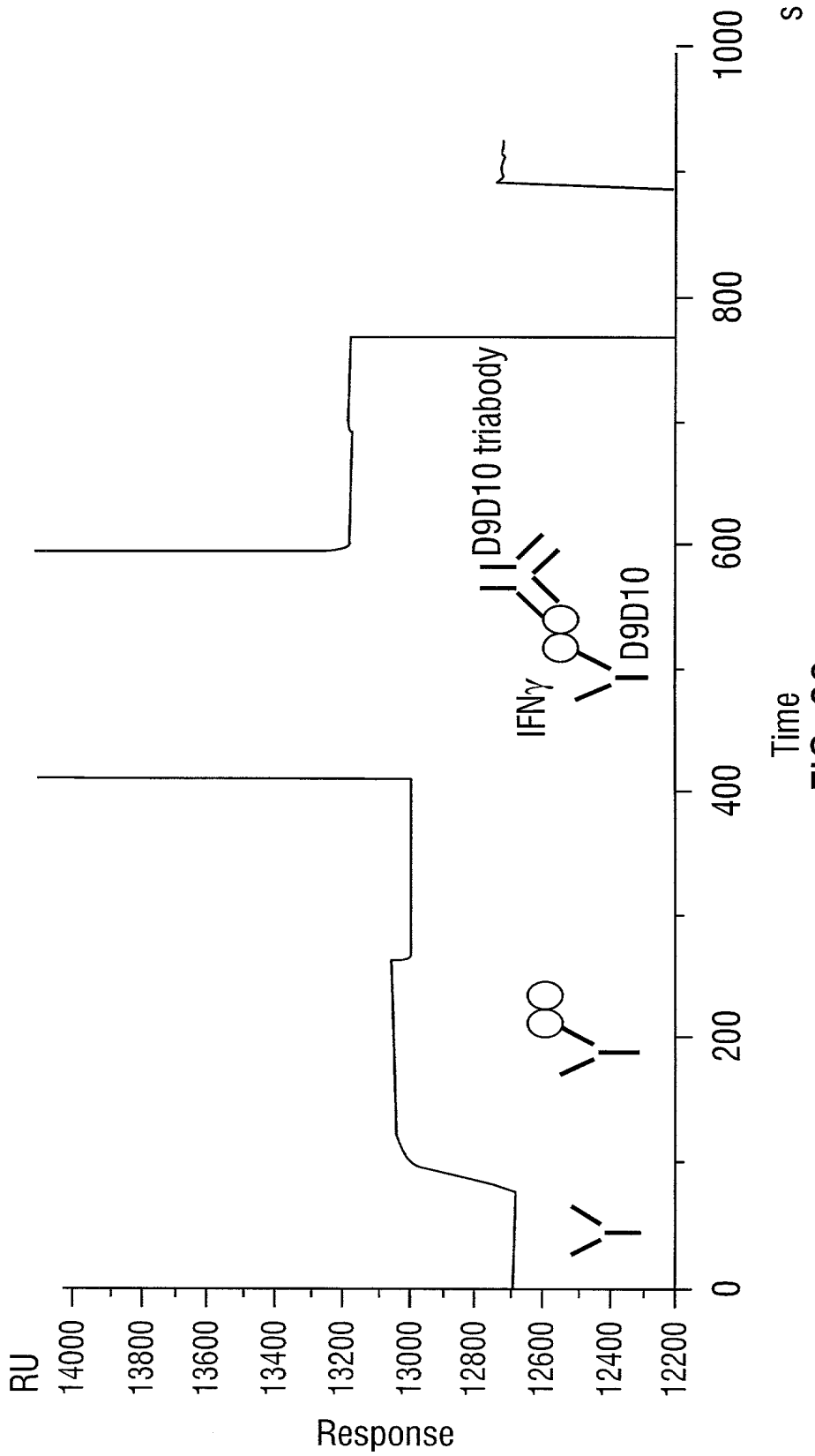
FIG. 26

```
  1  CAGGTGCAGCTGGTGCAGAGCGGTAGCGAACTGAAAAAACCGGGTGCGAG
 51  CGTTAAGATCAGCTGCAAAGCGAGCGGTTATACCTTCACCGATTACGGTA
101  TGAACTGGGTTAAACAGGCGCCGGGTCAAGGTCTGAAATGGATGGGTTGG
151  ATCAACACCTACACCGGTGAAAGCACCTACGTTGACGATTTCAAAGGTCG
201  TTTCGTTTTCAGCCTGGATACCAGCGTTAGCGCGGCCTACCTGCAGATCA
251  GCTCTCTGAAAGCGGAAGACACCGCGACCTACTTCTGCGCGCGTCGCGGT
301  TTCTACGCGATGGATTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTC
351  AGACATCGTACTGACCCAGAGCCCGGCGACCATGAGCGCGAGCCCGGGTG
401  AACGTGTTACCCTGACCTGCAGCGCGAGCTCTAGCATCAGCTATATGTTC
451  TGGTATCATCAGCGTCCGGGTCAGAGCCCGCGTCTGTTGATCTATGATAC
501  CAGCAACCTGGCGAGCGGTGTTCCGGCGCGTTTCAGCGGTAGCGGTAGCG
551  GTACCAGCTATAGCCTGACCATCAGCCGTATGGAACCGGAAGATTTCGCG
601  ACCTATTTCTGCCATCAGAGCTCTAGCTATCCGTTCACCTTCGGTCAGGG
651  TACCAAACTCGAGATCAAACGG
```

FIG. 27

```
1    QVQLVQSGSELKKPGASVKISCKASGYTFTDYGMNWVKQAPGQGLKWMGW
51   INTYTGESTYVDDFKGRFVFSLDTSVSAAYLQISSLKAEDTATYFCARRG
101  FYAMDYWGQGTTVTVSSDIVLTQSPATMSASPGERVTLTCSASSSISYMF
151  WYHQRPGQSPRLLIYDTSNLASGVPARFSGSGSGTSYSLTISRMEPEDFA
201  TYFCHQSSSYPFTFGQGTKLEIKRHHHHHH
```

FIG. 28


RU
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13600
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13000
12800
12600
12400
12200
Response
0
200
400
600
800
1000
s
Time
D9D10 triabody
IFNγ
D9D10

FIG. 29

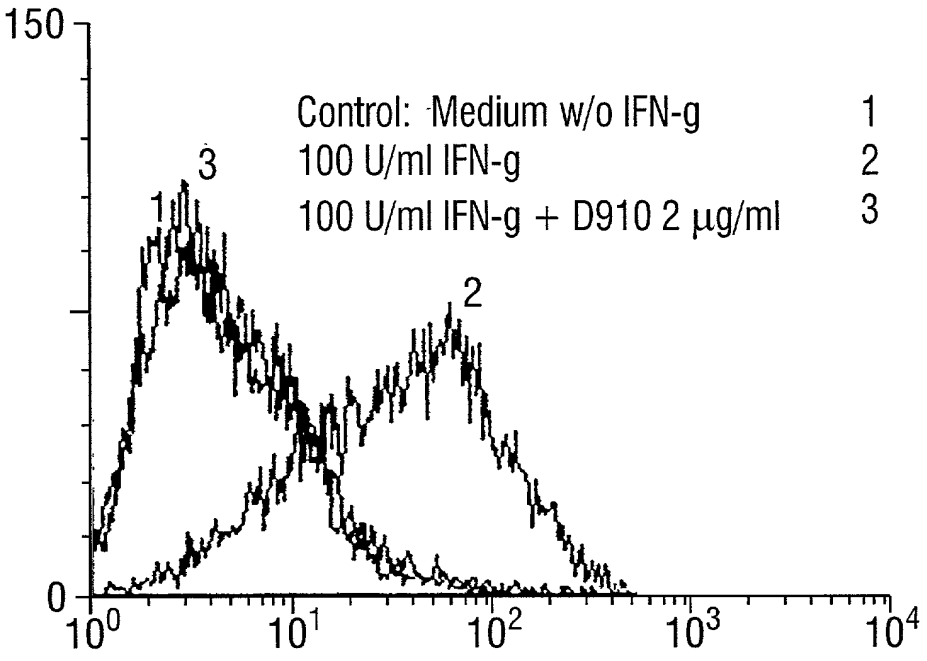

FIG. 30A

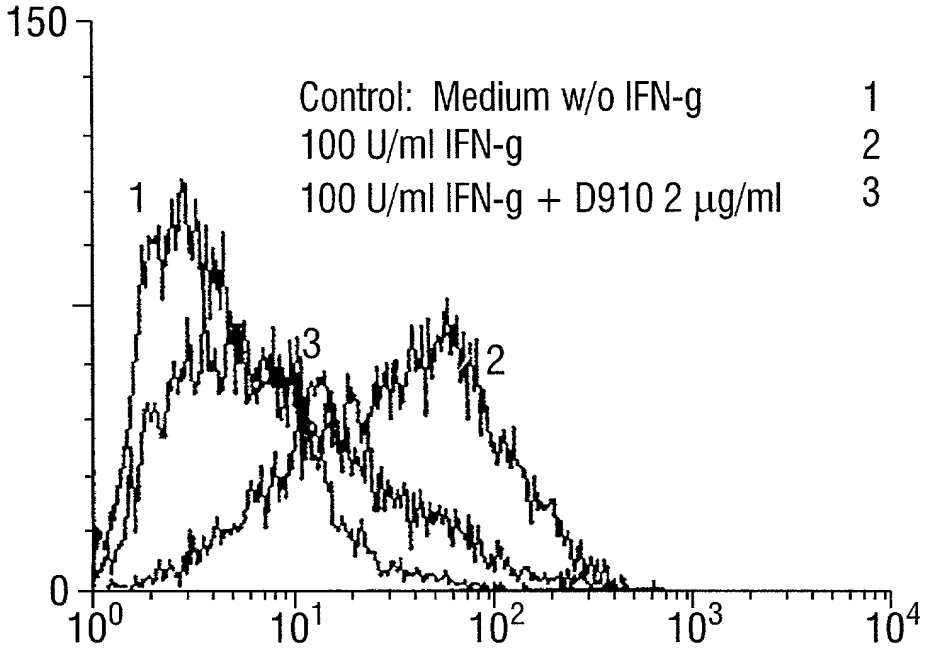

FIG. 30B

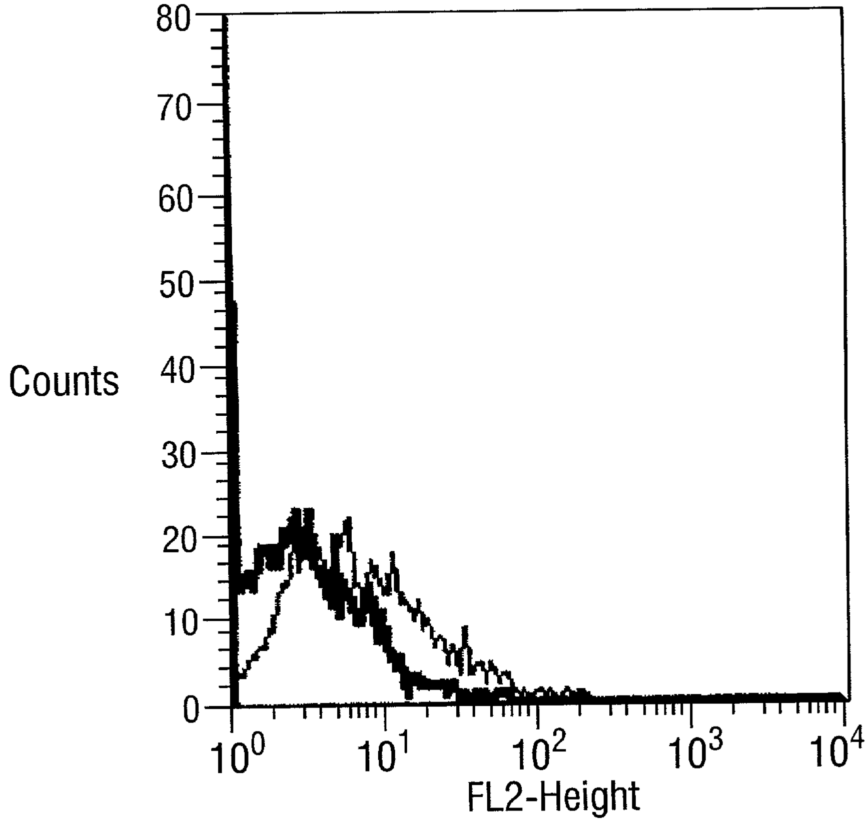

FIG. 31A

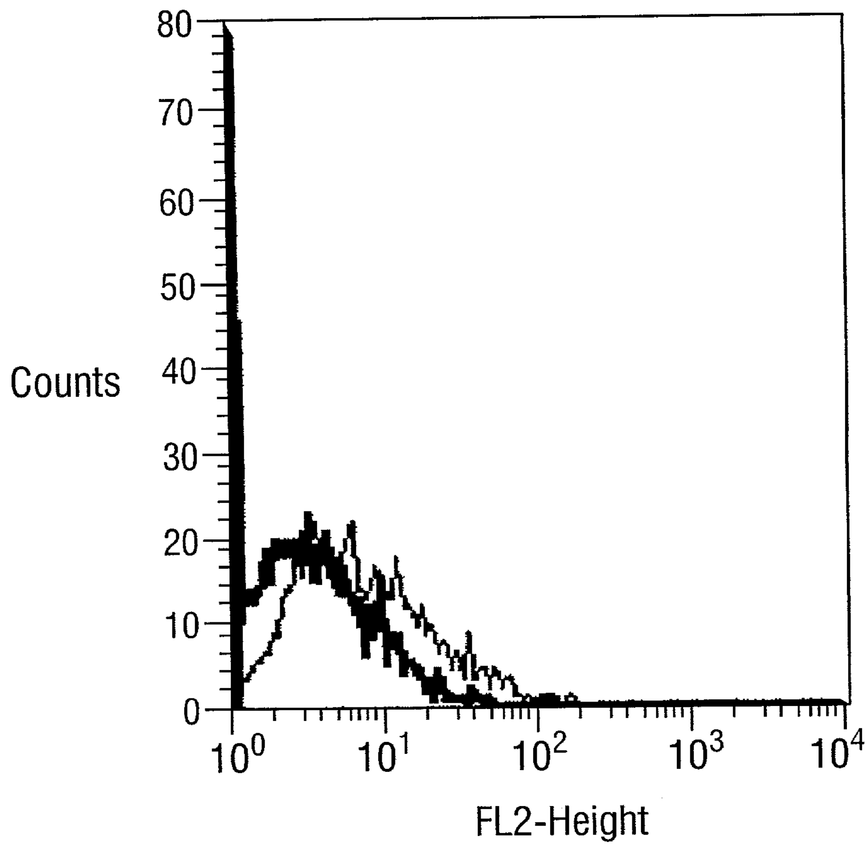

FIG. 31B

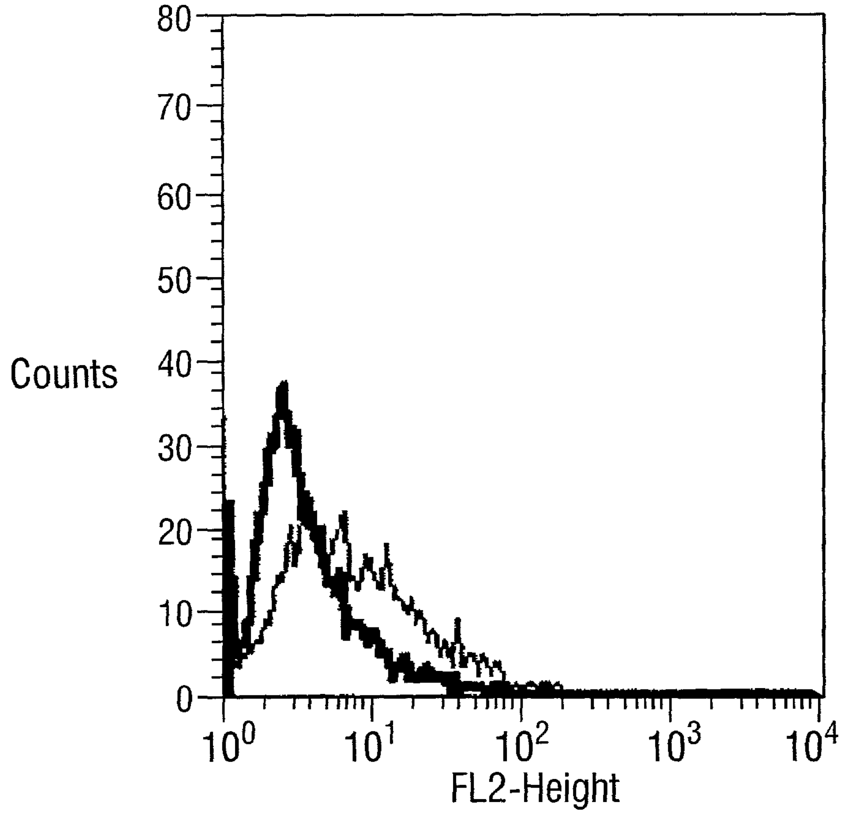

FIG. 31C

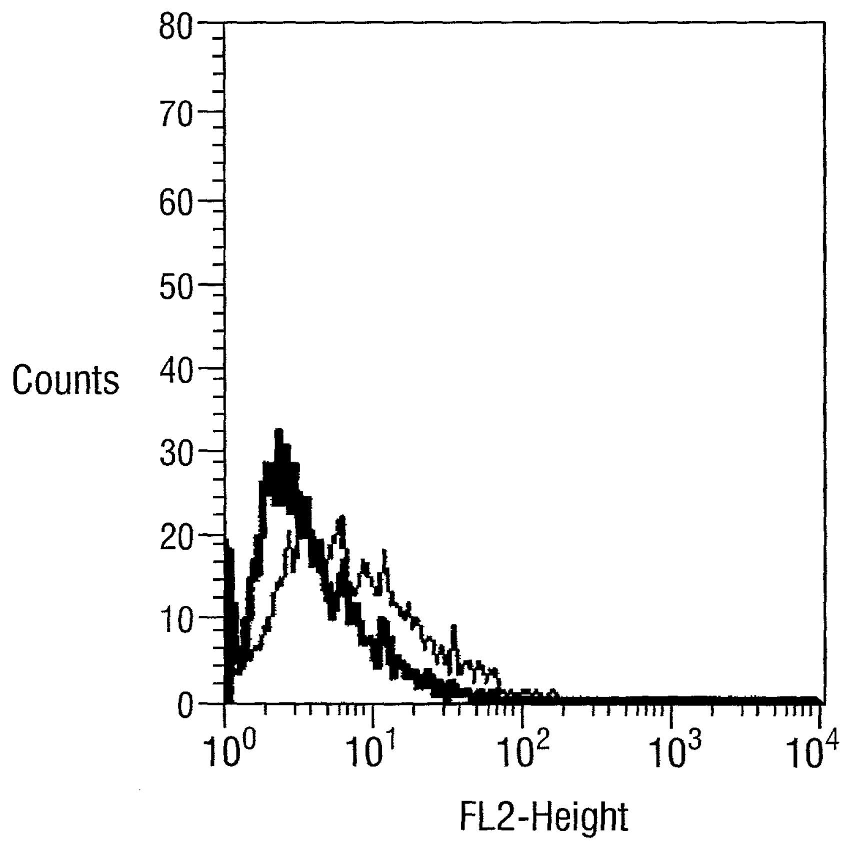

FIG. 31D

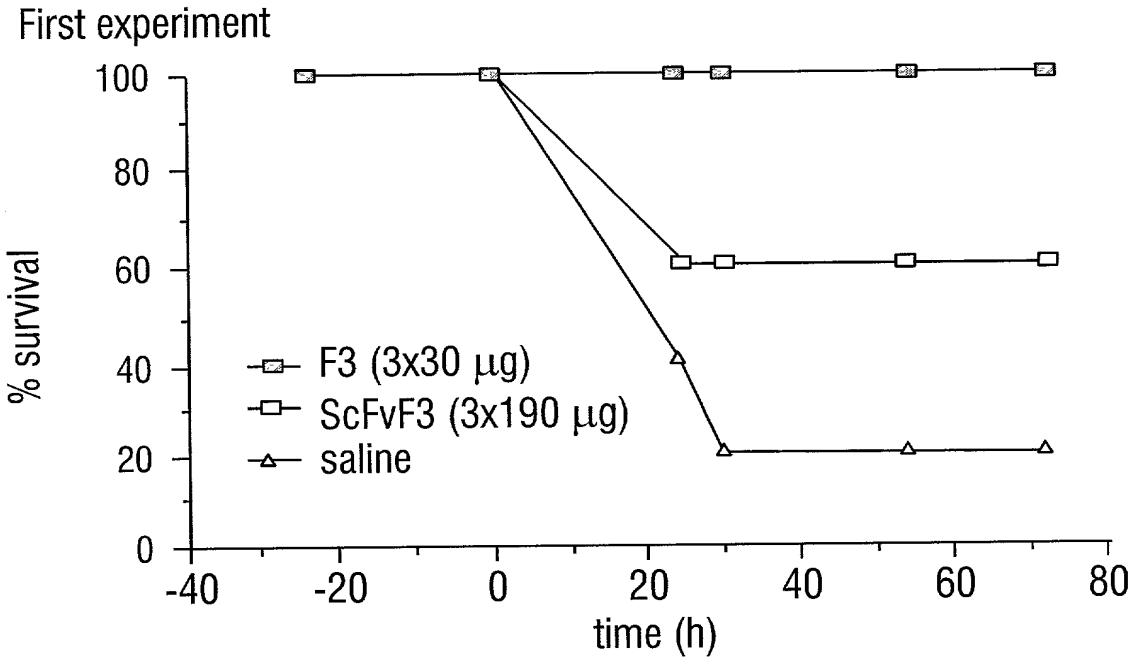

FIG. 32A

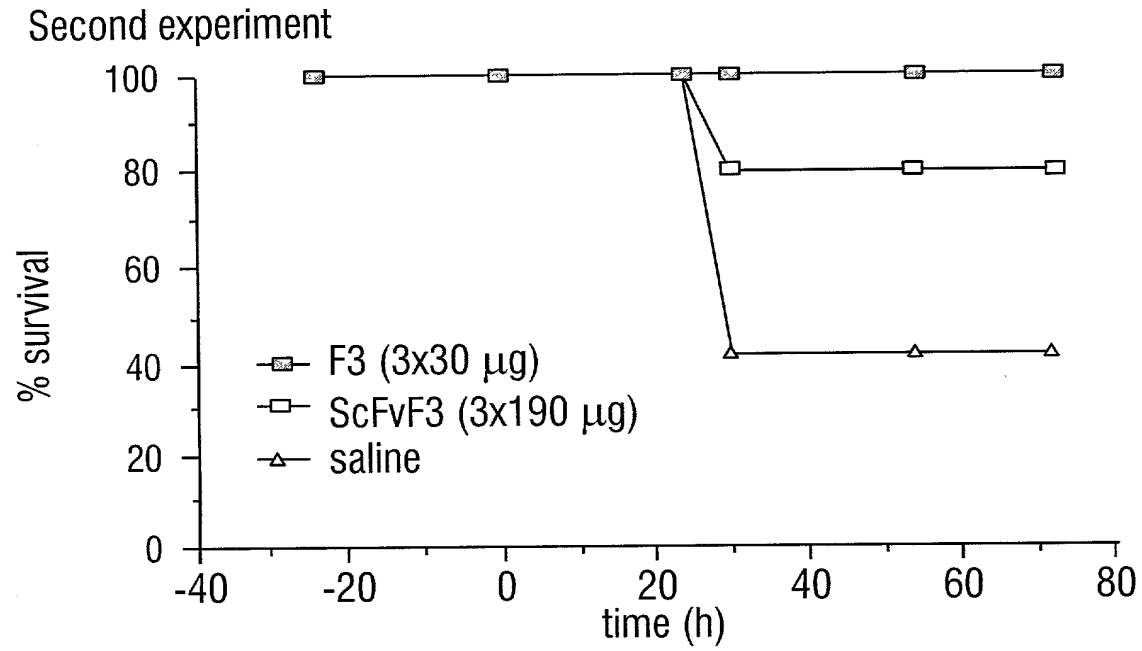

FIG. 32B

First experiment

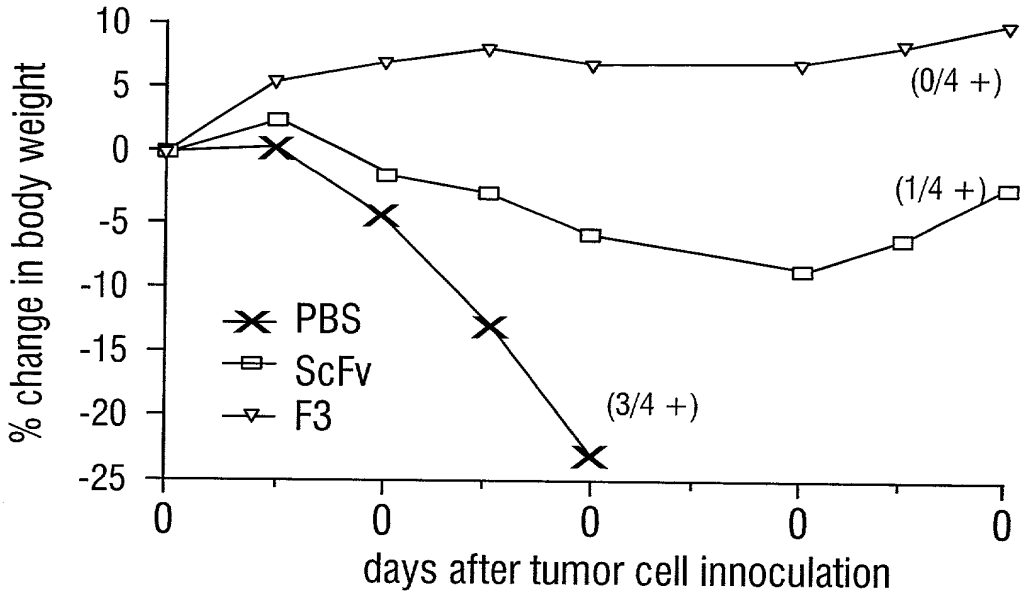

FIG. 33A

Second experiment

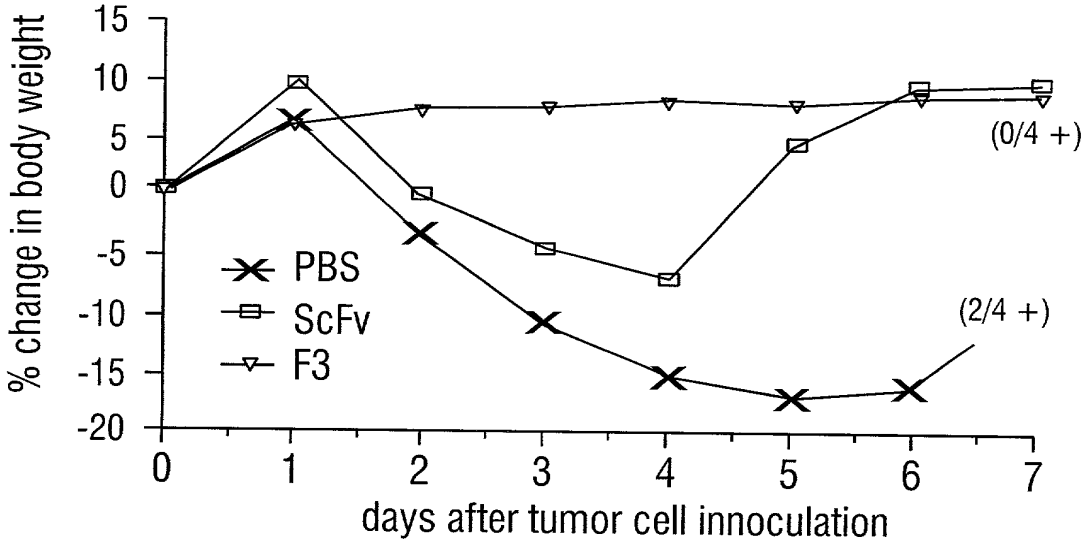

FIG. 33B